



results of BLAST

BLASTN 2.2.12 [Aug-07-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1132600206-2671-153796666945.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,579,719 sequences; 15,994,705,008 total letters

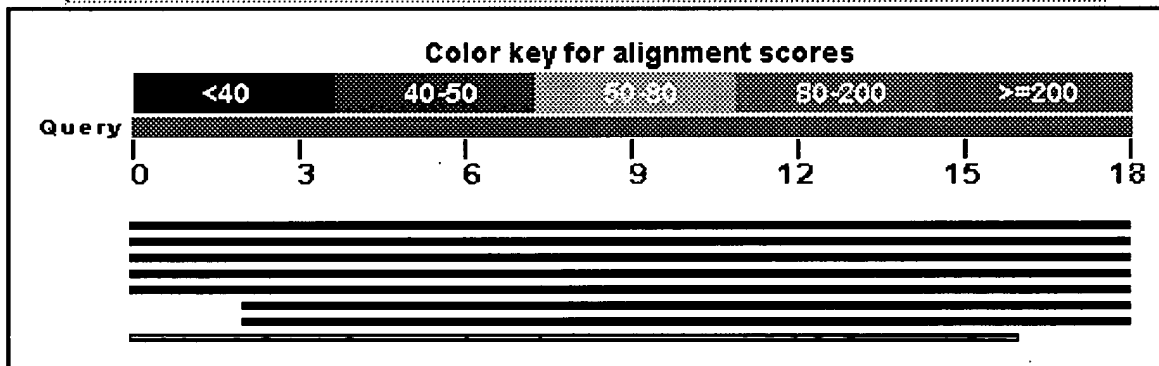
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=

(18 letters)

Distribution of 8 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Sequences producing significant alignments:		Score (Bits)	E Value
gi 33390917 qb AE017171.1 	Staphylococcus aureus plasmid pLW043,	36.2	0.41
gi 21886737 qb AF516335.1 	Enterococcus faecium plasmid pUW78...	36.2	0.41
gi 155036 qb M97297.1 TRNVAN	Enterococcus faecium transposon ...	36.2	0.41
gi 43335 emb X56895.1 EFPVANAG	E.faecium plasmid pIP816 vanA gen	36.2	0.41
gi 57790303 qb AY754011.1 	Enterococcus faecium vancomycin re...	36.2	0.41
gi 12666232 emb AL161898.17 	Human DNA sequence from clone RP...	32.2	6.4
gi 2370068 emb Z92540.1 HS179115A	Human DNA sequence from clo...	32.2	6.4
gi 479085 emb X79049.1 OTPDVANA2	O.turbata Plasmid DNA for vanco	32.2	6.4

Alignments

Get selected sequences

Select all

Deselect all

> ☐ [gi|33390917|gb|AE017171.1|](#) ☒ Staphylococcus aureus plasmid pLW043, complete sequence
Length=57889

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||
Sbjct 34773  CCGGTGGCAGCTACGTTT 34790
```

> ☐ [gi|21886737|gb|AF516335.1|](#) ☒ Enterococcus faecium plasmid pUW786 multiple antibiotic
gene cluster, complete sequence
Length=17510

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||
Sbjct 4222   CCGGTGGCAGCTACGTTT 4239
```

> ☐ [gi|155036|gb|M97297.1|TRNVAN](#) ☒ Enterococcus faecium transposon Tn1546 transposase
vanR (vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX),
vanY (vanY), and teicoplanin resistance protein (vanZ)
genes, complete cds
Length=10851

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||
Sbjct 7453   CCGGTGGCAGCTACGTTT 7470
```

> ☐ [gi|43335|emb|X56895.1|EFPVANAG](#) E. faecium plasmid pIP816 vanA gene for VANA ligase
Length=1768

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||
Sbjct 851    CCGGTGGCAGCTACGTTT 868
```

> ☐ [gi|57790303|gb|AY754011.1|](#) Enterococcus faecium vancomycin resistance protein A
partial cds
Length=614

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||||
Sbjct 241    CCGGTGGCAGCTACGTTT 258
```

> ☐ [gi|12666232|emb|AL161898.17|](#) ☒ Human DNA sequence from clone RP11-270H22 on chromosome
sequence
Length=122839

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query 3      GGTGGCAGCTACGTTT 18
             |||||
Sbjct 23455   GGTGGCAGCTACGTTT 23440
```

> ☐ [gi|2370068|emb|Z92540.1|HS179I15A](#) ☒ Human DNA sequence from clone RP1-179I15 on
a novel gene, a mitochondrial import receptor TOM22 pseudogene,
the 5' end of the KL gene for klotho, ESTs, STSs
and a CpG island, complete sequence
Length=146810

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query 3      GGTGGCAGCTACGTTT 18
             |||||
Sbjct 115256  GGTGGCAGCTACGTTT 115241
```

> ☐ [gi|479085|emb|X79049.1|OTPDVANA2](#) O.turbata Plasmid DNA for vancomycin resistance
Length=786

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGT 16
             |||||
Sbjct 345    CCGGTGGCAGCTACGT 360
```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental

samples or phase 0, 1 or 2 HTGS sequences)
Posted date: Nov 20, 2005 2:03 AM
Number of letters in database: -1,185,164,172
Number of sequences in database: 3,579,719
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 3579719
Number of Hits to DB: 281356
Number of extensions: 8869
Number of successful extensions: 8869
Number of sequences better than 10: 2
Number of HSP's better than 10 without gapping: 2
Number of HSP's gapped: 8869
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10: 8867
Length of query: 18
Length of database: 15994705008
Length adjustment: 16
Effective length of query: 2
Effective length of database: 15937429504
Effective search space: 31874859008
Effective search space used: 31874859008
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 11 (22.3 bits)
S2: 16 (32.2 bits)